In the Specification;

      Kindly amend the specification as follows.

      On page 1 of the specification, at line 6 immediately below the Title of the Invention, please insert the following paragraph:

      -- CROSS-REFERENCE TO RELATED APPLICATIONS

      This application is a divisional of U.S. Patent Application No. 09/692,081, filed October 19, 2000, which application is hereby incorporated by reference in its entirety herein. --

      Please delete the paragraph beginning at line 26 on page 30 and extending to line 11 on page 31, and replace it with the following amended paragraph:

      -- The determination of percent identity between two nucleotide or amino acid sequences can be accomplished using a mathematical algorithm. For example, a mathematical algorithm useful for comparing two sequences is the algorithm of Karlin and Altschul (1990, Proc. Natl. Acad. Sci. USA 87:2264-2268), modified as in Karlin and Altschul (1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). This algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990, J. Mol. Biol. 215:403410), and can be accessed, for example, at the National Center for Biotechnology Information (NCBI) world wide web site having the universal resource locator ~~"http://www.ncbi.nlm.nih.gov/BLAST/"~~ <<www.ncbi.nlm.nih.gov/BLAST/>>. BLAST nucleotide searches can be performed with the NBLAST program (designated "blastn" at the NCBI web site), using the following parameters: gap penalty =5; gap extension penalty=2; mismatch penalty =3; match reward =1; expectation value 10.0; and word size=11 to obtain nucleotide sequences homologous to a nucleic acid described herein. BLAST protein searches can be performed with the XBLAST program (designated "blastn" at the NCBI web site) or the NCBI "blastp" program, using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to obtain amino acid sequences homologous to a protein molecule described herein. –

2

Please delete the paragraph at lines 12-18 on page 31 and replace it with the following amended paragraph:

-- To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402). Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules (id.) and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped BLAST, PSI-Blast, and PHI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See ~~http://www.ncbi.nlm.nih.gov~~ <<www.ncbi.nlm.nih.gov>>. --

Please delete the paragraph at lines 16-21 on page 109 of the specification and replace it with the following amended paragraph:

-- Partial sequences of approximately 300 clones were obtained by automated sequencing and the sequence identities were determined by searching GenBank databases, including non-redundant and EST (expressed sequence tag) databases which are publicly available at ~~http://www.ncbi.nlm.nih.gov/blast/blast.cgi~~ << www.ncbi.nlm.nih.gov/blast/blast.cgi>>. Those sequences not matching a known gene (usually corresponding murine or human ESTs) were identified in the database and were pursued further. --

Please delete the paragraph beginning at line 27 on page 111 and extending to line 12 on page 112, and replace it with the following amended paragraph:

-- Searching The Institute for Genomic Research (TIGR) sequence database for the human homolog of REMODEL, identified a 771 bp of 3' sequence. Using RNA from cultured human aortic SMC, 5' RACE (rapid amplification of cDNA ends) cloning was performed to identify the missing approximately 500 bp sequence located at the 5' end. The sequence alignment of rat (SEQ ID NO:2) and human REMODEL (SEQ ID NO:4) is shown in FIG. 4. Interestingly, the human sequence did not have the additional 5' AUG translational start

3

site but only contained the AUG codon at position 114. A 5' primer located upstream of this AUG start site and a 3' primer were designed to verify that the AUG start site at position 19 of the rat sequence was not a cloning artifact. Reverse transcription polymerase chain reaction (RT-PCR) analysis and sequencing was performed to confirm the presence of the AUG-19 codon. The overall identity between the human and rat REMODEL sequence was 78.3% at the nucleotide level using a blast 2 algorithm search as provided at the web site ~~http://www.ncbi.nlm.nih.gov/gorf/b12.html~~ << www.ncbi.nlm.nih.gov/gorf/b12.html>>, which web site is publicly available. Further, homology between the rat (SEQ ID NO:2) and human REMODEL (SEQ ID NO:4) amino acid sequences is greater than about 97% using the blast 2 algorithm search strategy described previously. --